



## FIG. 1A

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      11      20      29      38      47      56
5'  GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT
      -----
      65      74      83      92      101      110
    ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA
      -----
            M   E   S   R   K   D   I   T   N   Q   E   E   L   W   K

      119      128      137      146      155      164
    ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA
      -----
            M   K   P   R   R   N   L   E   E   D   D   Y   L   H   K   D   T   G

      173      182      191      200      209      218
    GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT
      -----
            E   T   S   M   L   K   R   P   V   L   L   H   L   H   Q   T   A   H

      227      236      245      254      263      272
    GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA
      -----
            A   D   E   F   D   C   P   S   E   L   Q   H   T   Q   E   L   F   P

      281      290      299      308      317      326
    CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT
      -----
            Q   W   H   L   P   I   K   I   A   A   I   I   A   S   L   T   F   L

      335      344      353      362      371      380
    TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT
      -----
            Y   T   L   L   R   E   V   I   H   P   L   A   T   S   H   Q   Q   Y

      389      398      407      416      425      434
    TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC
      -----
            F   Y   K   I   P   I   L   V   I   N   K   V   L   P   M   V   S   I

      443      452      461      470      479      488
    ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT
      -----
            T   L   L   A   L   V   Y   L   P   G   V   I   A   A   I   V   Q   L

      497      506      515      524      533      542
    CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA
      -----
            H   N   G   T   K   Y   K   K   F   P   H   W   L   D   K   W   M   L

      551      560      569      578      587      596
    ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT
      -----
            T   R   K   Q   F   G   L   L   S   F   F   F   A   V   L   H   A   I

      605      614      623      632      641      650
    TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG
      -----
            Y   S   L   S   Y   P   M   R   R   S   Y   R   Y   K   L   L   N   W
  
```

## REPLACEMENT SHEET

659	668	677	686	695	704
GCA TAT CAA CAG GTC	CAA CAA AAT AAA	GAA GAT GCC TGG	ATT GAG CAT GAT	GTT	
-----					
A Y Q Q V Q Q N K E D A W I E H D V					
713	722	731	740	749	758
TGG AGA ATG GAG ATT	TAT GTG TCT CTG	GGA ATT GTG GGA	TTG GCA ATA CTG	GCT	
-----					
W R M E I Y V S L G I V G L A I L A					
767	776	785	794	803	812
CTG TTG GCT GTG ACA	TCT ATT CCA TCT	GTG AGT GAC TCT	TTG ACA TGG	AGA GAA	
-----					
L L A V T S I P S V S D S L T W R E					
821	830	839	848	857	866
TTT CAC TAT ATT CAG	AGC AAG CTA GGA	ATT GTT TCC CTT	CTA CTG GGC	ACA ATA	
-----					
F H Y I Q S K L G I V S L L L G T I					
875	884	893	902	911	920
CAC GCA TTG ATT TTT	GCC TGG AAT AAG	TGG ATA GAT ATA	AAA CAA TTT	GTA TGG	
-----					
H A L I F A W N K W I D I K Q F V W					
929	938	947	956	965	974
TAT ACA CCT CCA ACT	TTT ATG ATA GCT	GTT TTC CTT CCA	ATT GTT GTC	CTG ATA	
-----					
Y T P P T F M I A V F L P I V V L I					
983	992	1001	1010	1019	1028
TTT AAA AGC ATA CTA	TTC CTG CCA TGC	TTG AGG AAG AAG	ATA CTG AAG	ATT AGA	
-----					
F K S I L F L P C L R K K I L K I R					
1037	1046	1055	1064	1073	1082
CAT GGT TGG GAA GAC	GTC ACC AAA ATT	AAC AAA ACT GAG	ATA TGT TCC	CAG TTG	
-----					
H G W E D V T K I N K T E I C S Q L					
1091	1100	1109	1118	1127	1136
TAG AAT TAC TGT TTA	CAC ACA TTT TTG	TTC AAT ATT GAT	ATA TTT TAT	CAC CAA	
-----					
* N Y C L H T F L F N I D I F Y H Q					
1145	1154	1163	1172	1181	1190
CAT TTC AAG TTT GTA	TTT GTT AAT AAA	ATG ATT ATT CAA	GGA AAA AAA	AAA AAA	
-----					
H F K F V F V N K M I I Q G K K K K					

AAA AA 3' SEQ ID NO:1

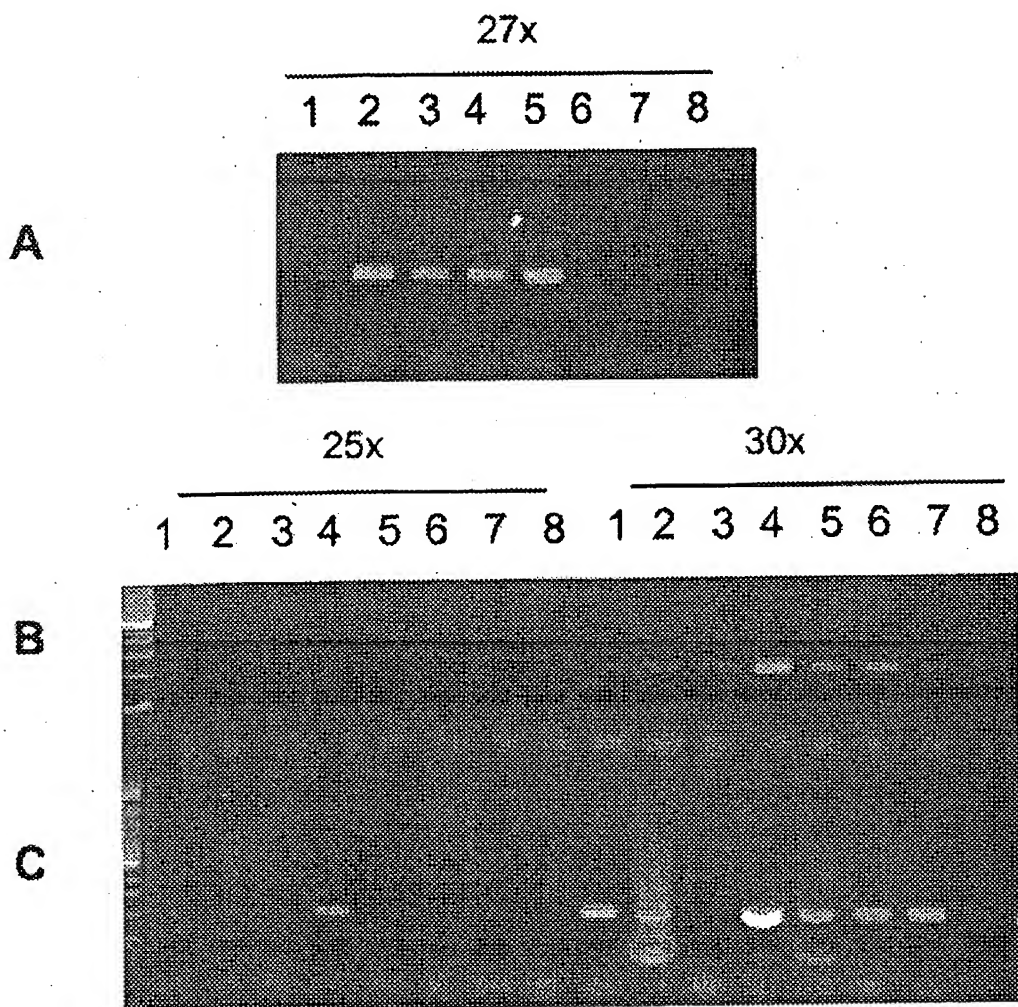
K

SEQ ID NO:2

**FIG. 1C**

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG  
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT  
AAC AGC AAG 3' SEQ ID NO:3

FIG. 2



## Panels:

**A**

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

**B**

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

**C**

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

## FIG. 4

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC  
ATACTATTTTATAGAATTAATGGAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG  
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC  
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACA  
GTGGCACTTGCCAATTAATAAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT  
CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG  
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTCATAATGGAACCAA  
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT  
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT  
ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT  
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG  
AGAGAATTTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT  
ATAGAATATGTTGACTTTACCCCATAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT  
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTCCTAGACATAAATAAAGGCAT  
TAAATATTCTTTGTTTTTTTTTTTTGTTTGTGTTGTTTTGTTTGTGTTGTTTTGAGATGAAGTCTCG  
CTCTGTTGCCCATGCTGGAGTACAGTGGCAGCATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATT  
TCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTAGTA  
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC  
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCTGCTCTTCTAATATTTGAAACTTGTTAGACAATTT  
GCTACCCATCTAATGTGATATTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAATATTCTTTTACC  
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTTAGCACTTCCAGAAACAAAACTCTCTCCTTGAAA  
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT  
ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT  
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAA  
TTTAATTCAGTCATGAACACTGCCAATTACCGTTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT  
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC  
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCTTAATTTTGTAGGTTTCTAG  
CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA  
TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACCTGAGCCTATTCTACTATATGTACA

ATACCTAGCCCATAAAGGTATACAATACACATTTGGTAAACTAATTTTCAACCAATGACATGTATTTTCAACT  
AGTAACCTAGAAATGTTTCACTTAAAATCTGAGAAGTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA  
ACGCAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTTCGATTTGTTCT  
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT  
TGAGATTACATAGGTGAACAACTATTTTAAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA  
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC  
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTTCATTATCAAAATCAGAGTGAATCA  
CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTGTCTATAATCTTCAATCTACCTATAT  
TTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGTATAAGTAAGACTCAGTCCCT  
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAATAAATATCATAAG  
GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG  
TTCACCTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG  
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG  
ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTCTTTTGAGAGCAAGCTAGGA  
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG  
TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATT  
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAAGTGAAG  
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FIG. 5

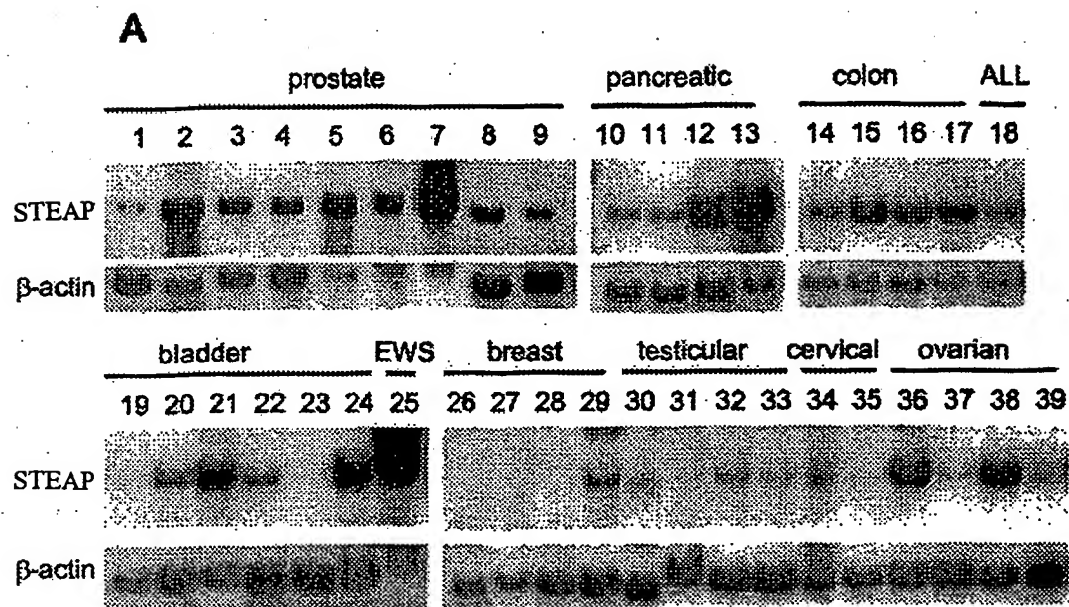
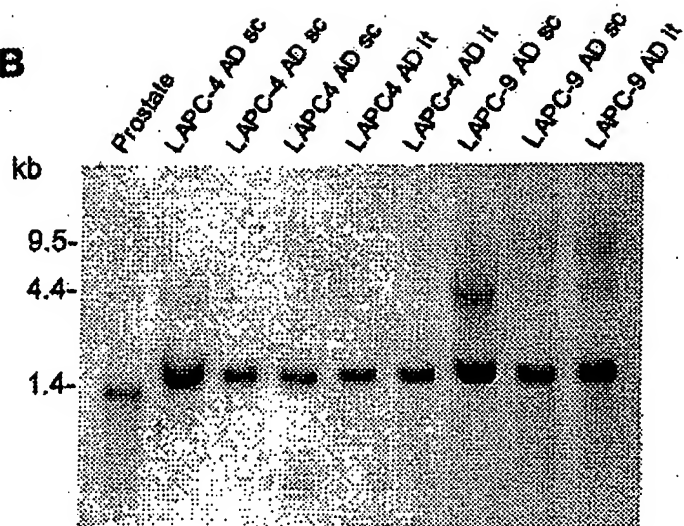
**B**

FIG. 6

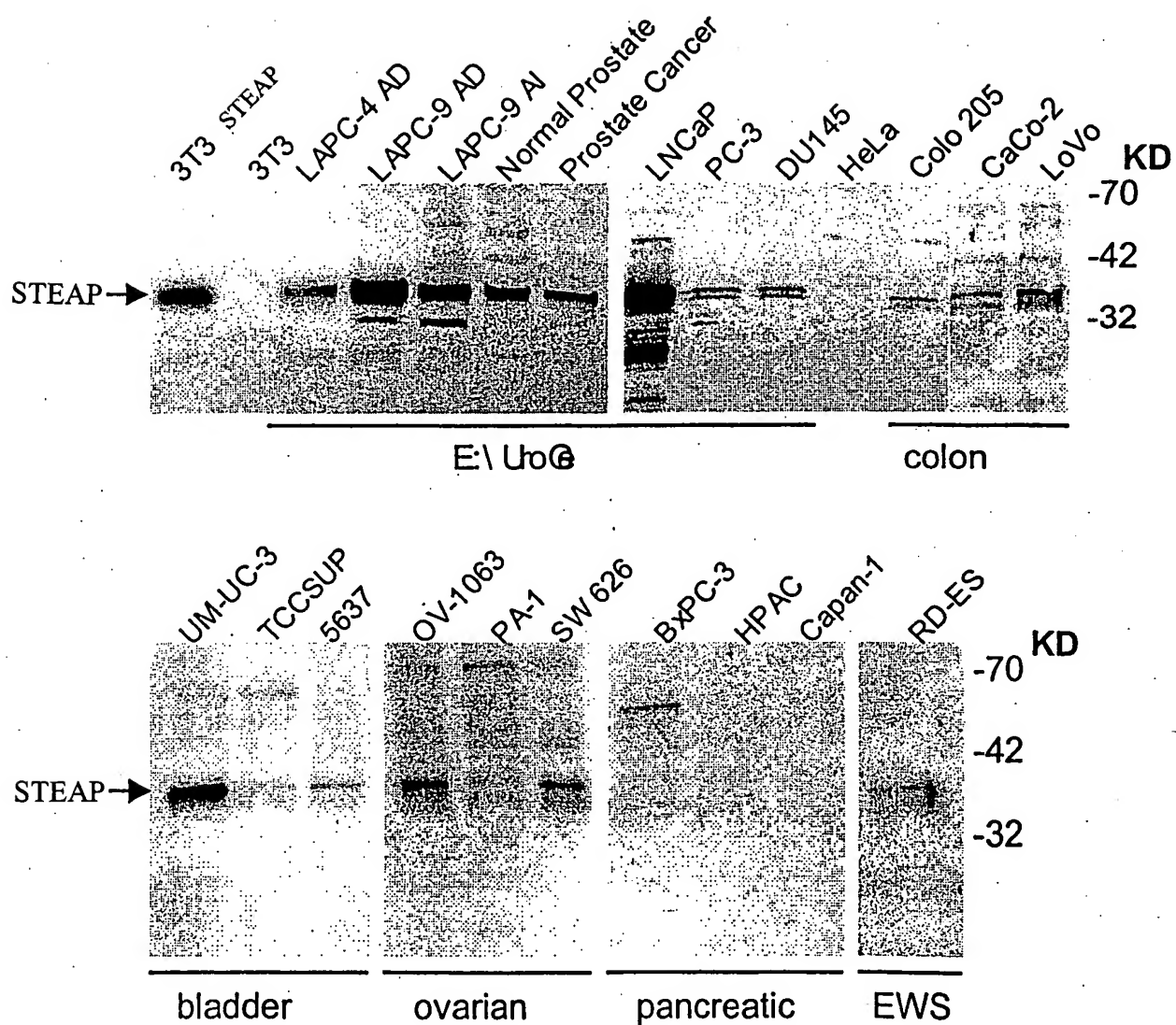






FIG. 9

	10	19	28	37	46	55
5'	GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT ATA GTT GCC					
	Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile Val Ala					
	64 73 82 91 100 109					
	ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA GGT CTT CTG GCA GCT GCT TAT CAA					
	Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala Ala Ala Tyr Gln					
	118 127 136 145 154 163					
	CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA ACC TGG TTA					
	Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu					
	172 181 190 199 208 217					
	CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG GTC CAT GTT					
	Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val					
	226 235 244 253 262 271					
	GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG TTT CTC AAC					
	Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn					
	280 289 298 307 316 325					
	ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT GAG GAA GAA					
	Met Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu					
	334 343 352 361 370 379					
	GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT GGC TTA CTT					
	Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu					
	388 397 406 415 424 433					
	TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA AAC TGG AGA					
	Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg					
	442 451 460 469 478 487					
	GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC ATA AGT ACT					
	Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile Ser Thr					
	496 505 514					
	TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT 3' SEQ ID NO:7					
	Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala SEQ ID NO:8					

## FIG. 10

STEAP-2, AA508880 (NCI\_CGAP Pr6) SEQ ID NO:9

ggtcgacttttccctttattccctttgtcagagatctgattcatccatattgctagaaaccaacagagtgacttttaca  
aaattccctatagagattgtgaataaaaaccttacctatagttgccattactttgtctctccctagtataaccttgcagg  
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttgggtggaaacctggta  
cagtgtagaaaacagcttggattactaagttgtttcttcgctatgggccatgttgcctacagcctctgcttaccga  
tgagaagggtcagagagat

STEAP-2, 98P4B6 SSH fragment SEQ ID NO:10

TTTGCGCTTTGCAGATACCCAGACTGAGCTGGAATTTGTCTTCCTATTGACTCTACTTCTTTAAAGCG  
GCTGCCCATTAATTCTCAGCTGTCCTTGCACTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC  
TCCTCAAAGGAAGGCAGCATGTGTCCTTTT

AI139607 (testis EST) SEQ ID NO:11

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttgggtttt  
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcactggagagagtccgatattgt  
ccagtcctaaactgggttatttgacctgatcttgtgtacagcccacacctgggtgtacggtgggaagagattcctc  
agcccttcaaatctcagatgggtatcttctcgcagcctacgtgttagggcttatcattccttgcactgtgctgggtga  
tcaagtttgcctaatcatgccatgtgttagacaaacaccttacaaggatccgccagggtgggaagggaactcaaa  
acactagaaaaagcatggaatggaaaatcaatatttaaaacaaagttcaatttagctggaaaaaaaaa

R80991 (placental EST) SEQ ID NO:12

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aaggaggaggtctggcggtggagatctacctctccctgggagtgctggccctcggcacgttgctccctgctggcg  
tgacctcactgccgtccattgcaaaactcgtcaactggaggaggttcagcttcggttcagtcctcactgggtttgt  
ggcctcgtgctgagcacactncacacgctcacctacggctggaccgcgccttcgaggagagccgctacaagttc  
tacctnctcccaccttcacgntcacgctgctgggtgcctcggttcggttcacctgggccaagccctgttntac  
tgcttgcattcagccgnaga

## FIG. 11A

STEAP-1	106	FYKIPILVINKVLPVVSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKMWLTKQFG	
STEAP-2	2	FYKIPIEIVNKTLPPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLG	
		*****	***
STEAP-1	166	LLSFFFVAVLHAIYSLSPMRRSYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIV	
STEAP-2	62	LLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIM	
		*****	***
STEAP-1	226	GLAILALLAVTSIPSVSDSLTWREPHYIQSKLGIVSLLLGTIHALIFAWNK	PORTION OF SEQ ID NO:2
STEAP-2	122	SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR	PORTION OF SEQ ID NO:8
		* * *	

**FIG. 11B**

	271	285	286	300	301	315	316	330	331	345	346	360
STEAP-1	IPAWNKWIDIKQFVW	YTPPTF	MLAVFLPIV	VLIFPKSILFLPCL	ARK	KILKIR	HCSE	EDVTKI	NKTEICSQL	339	SEQ ID NO:2	
STEAP-2	YIGWTRA									173	SEQ ID NO:8	
STEAP-3	YIGGKRFLSPSNLKW	YLPAAV	VLGLIIPCT	VLV	IKFVLIMPCVDN	TLTRIR	PCSE	ERNSKH		128	SEQ ID NO:33	
STEAP-4	TYGNTRAFEESERYKF	YLPPTFT	TXTLVPCV	RSSWAKALFXLPCIQ	P					128	SEQ ID NO:34	

FIG. 17

